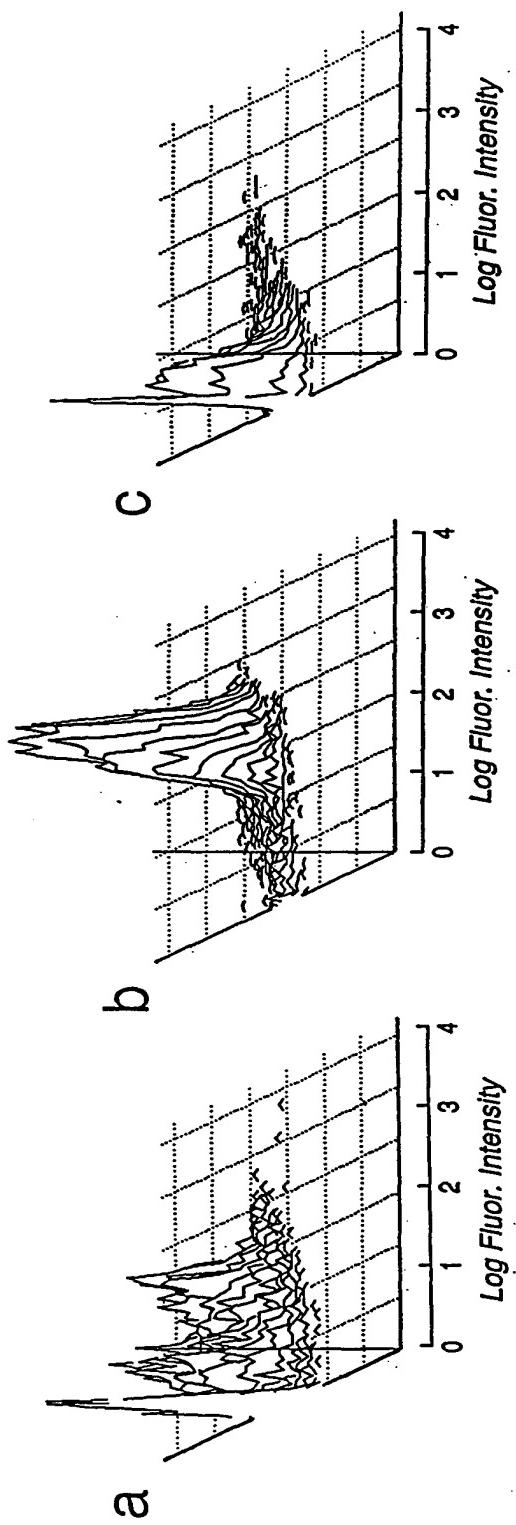


FIGURE 1

FIGURE 2



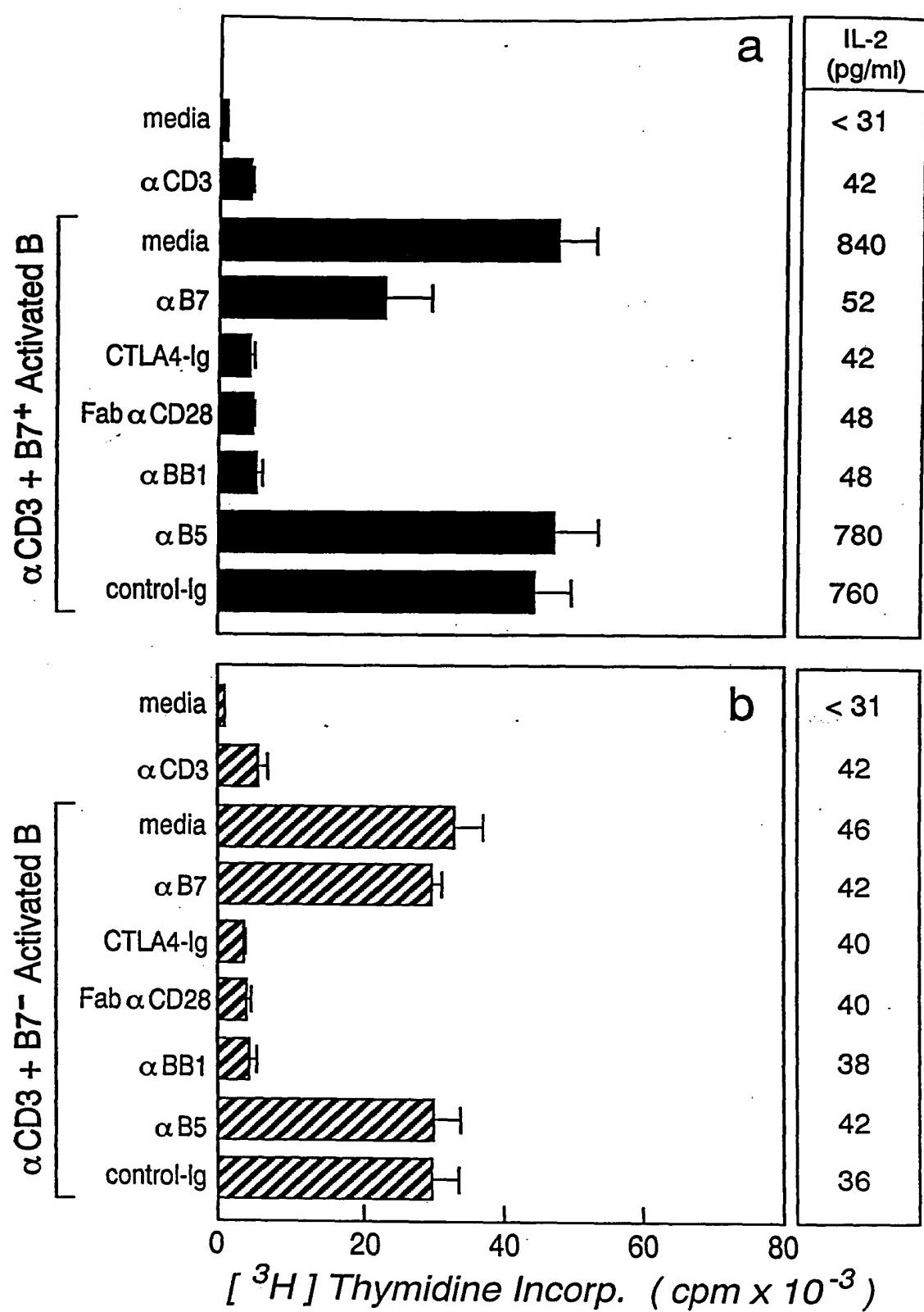


FIGURE 3

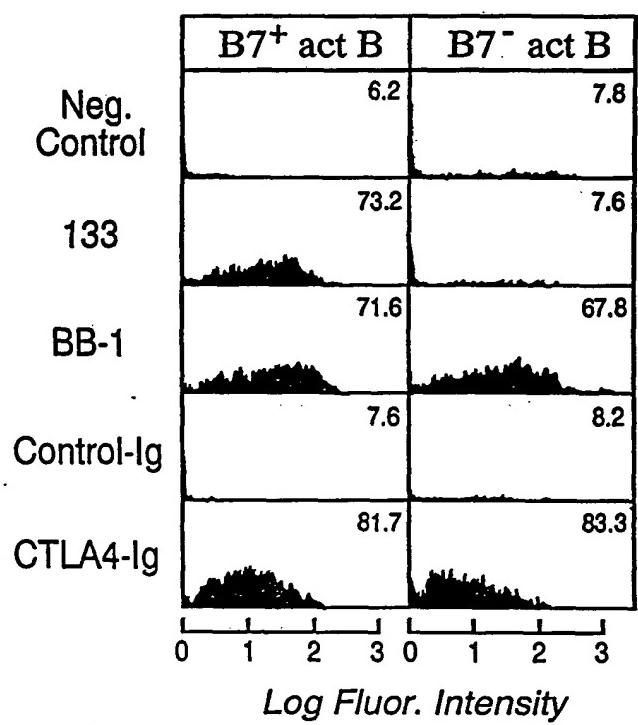


FIGURE 4

B Cells Activated by sIg Crosslinking

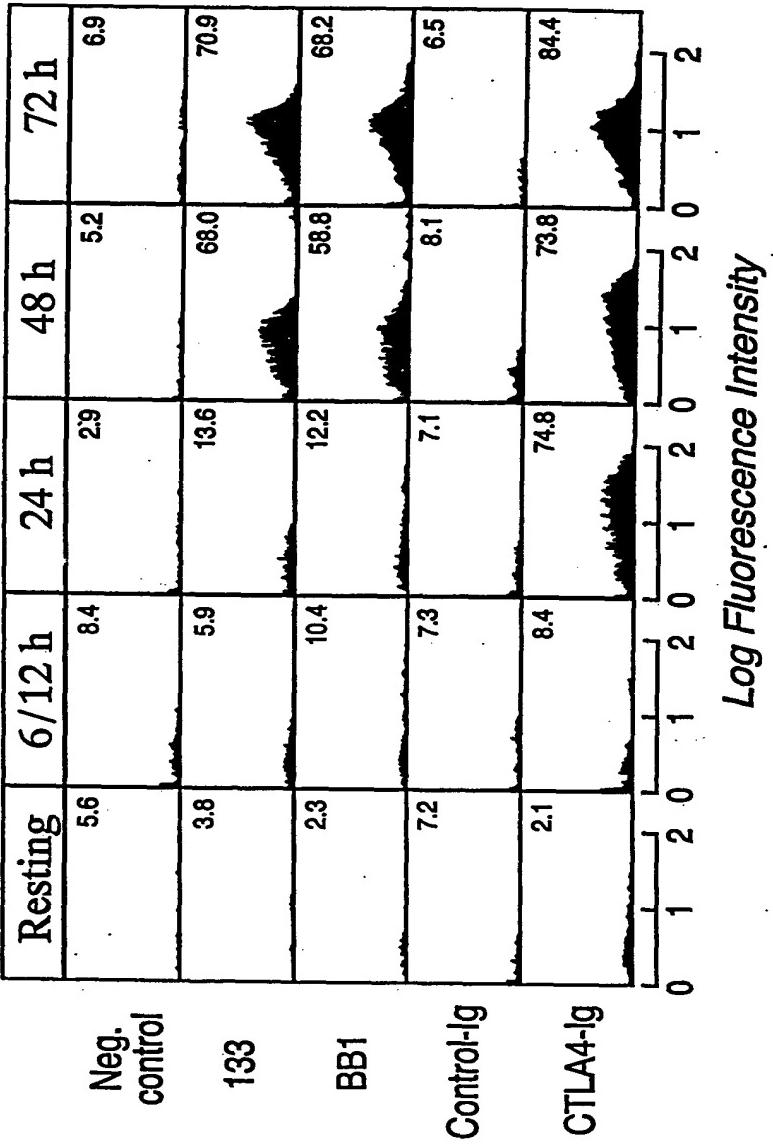


FIGURE 5

B Cells Activated by Class II Crosslinking

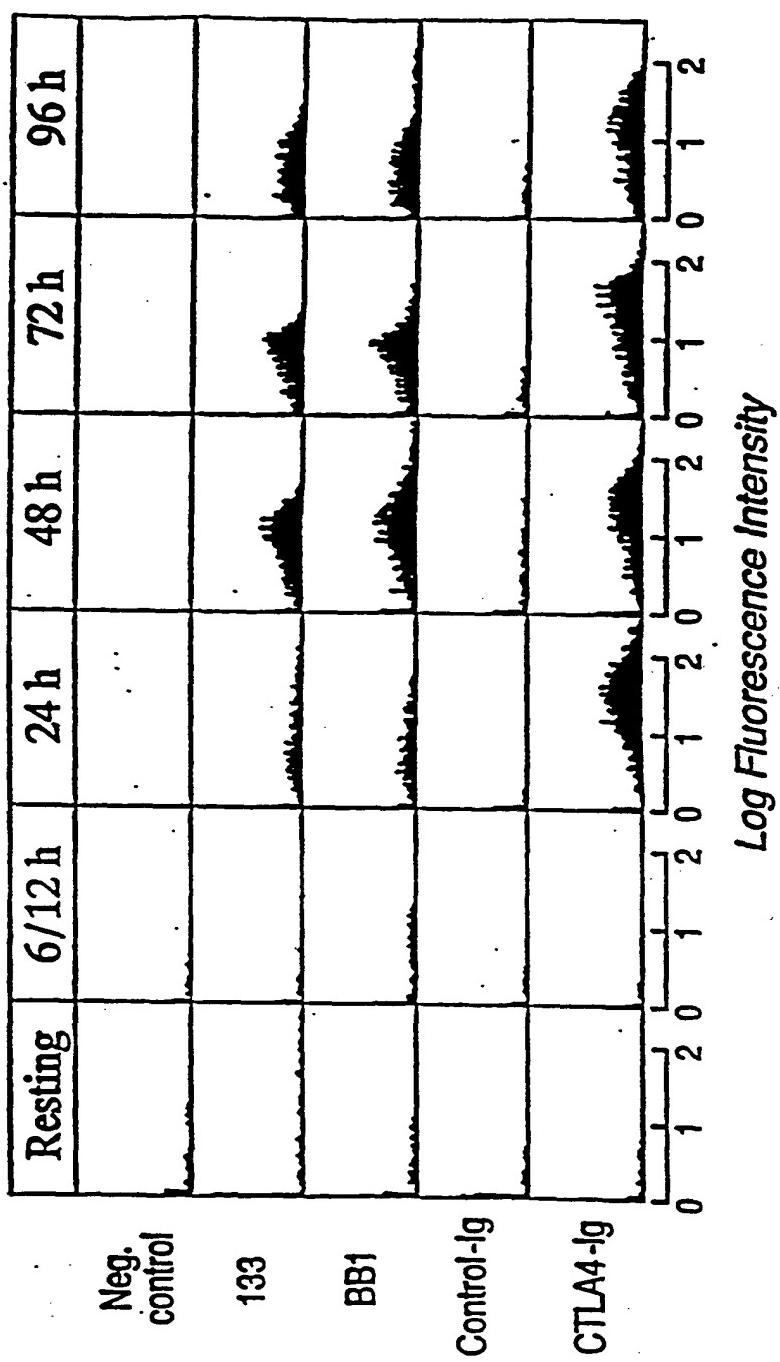


FIGURE 6

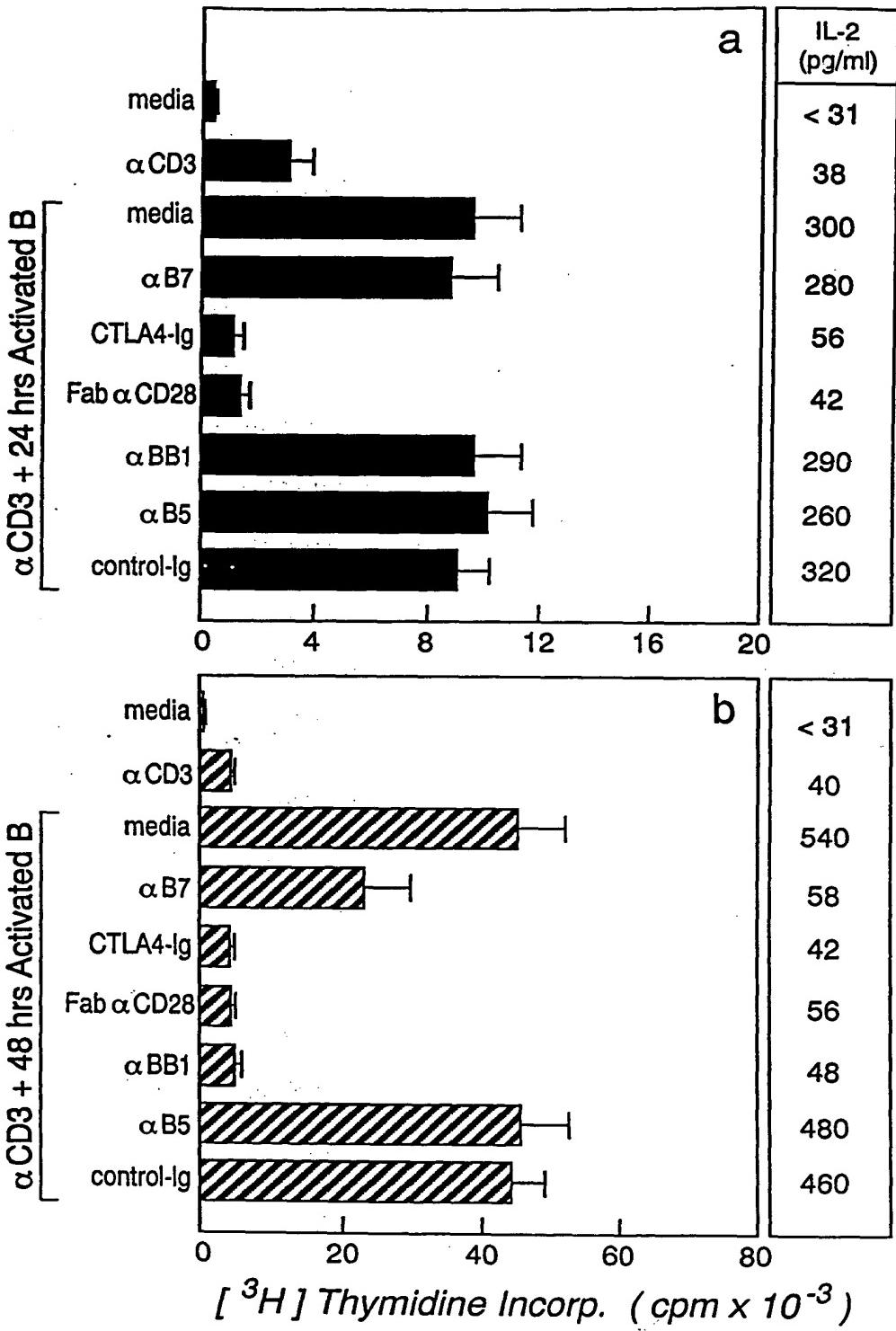


FIGURE 7

1	CACAGGGTGAAGCTTGCCTCTGCTGCTGTAACAGGGACTAGCACAGACACACGGATGAGTGGGTC	70
71	ATTCCAGATATTAGGTACAGCAGCAAAATGGATCCCCAGTGCACATGGACTGAGTAACA	140
	M D P Q C T M G L S N	11
141	TTCTCTTGTGATGGCCTTCCTGCTCTGGTGCTCGCTCTGAAGATTCAAGCTTATTCAATGAGAC	210
12	I L F V M A F L L S G A A A P L K I Q A Y F N E T	35
	^ #	
211	TGCAGACCTGCCATGCCAATTGCAAACCTCTCAAAACCAAGCCTGAGTAGCTAGTAGTATTGGCAG	280
36	A D L P C Q F A N S Q N Q S L S E L V V F W Q	58
	* #	
281	GACCAGGAAAACCTGGTTCTGAATGAGGTATACTTAGGCAAAGAGAAATTGACAGTGTTCATTCCAAGT	350
59	D Q E N L V L N E V Y L G K E K F D S V H S K	81
351	ATATGGGCCGCACAAGTTTGATCGGACAGTTGGACCCCTGAGACTTCACAATCTCAGATCAAGGACAA	420
82	Y M G R T S F D S D S W T L R L H N L Q I K D K	105
421	GGGCTTGTATCAATGTATCATCCATCACAAAAAGCCCACAGGAATGATTCCGCATCCACCAGATGAATTCT	490
106	G L Y Q C I I H H K K P T G M I R I H Q M N S	128
	* #	
491	GAAC TGTCAGTGCTTGTAACTTCAGTCACCTGAAATAGTACCAATTCTAATATAACAGAAAATGTGT	560
129	E L S V L A N F S Q P E I V P I S N I T E N V	151
	# #	
561	ACATAAAATTGACCTGCTCATCTACACGGTTACCCAGAACCTAACAGAAGATGAGTGTGCTAACAC	630
152	Y I N L T C S S I H G Y P E P K K M S V L L R T	175
	# *	
631	CAAGAATTCAACTATCGAGTATGGTATTATGCAGAAATCTCAAGATAATGTCACAGAACTGTACGAC	700
176	K N S T I E Y D G I M Q K S Q D N V T E L Y D	198
	# #	
701	GTTTCCATCAGCTTGTCTGTTCAATTCCCTGATGTTACGAGCAATATGACCATCTTCTGTATTGGAAA	770
199	V S I S L S V S F P D V T S N M T I F C I L E	221
	# *	
771	CTGACAAGACGGCTTTATCTCACCTTCTCTATAGAGCTTGAGGACCCCTCAGCCTCCCCAGACCA	840
222	T D K T R L L S S P F S I E L E D P Q P P P D H	245

FIGURE 8A

841	CATTCCTTGGATTACAGCTGTAC	CCAAACAGTTATTATATGTGTGATGGTTTCTGTCTAATTCTATGG	910
246	<u>I P W I T A V L P T V I I C V M V F C L I L W</u>		268
911	AAATGGAAGAAGAAGAAGCGGCCTCGCAACTCTTATAAATGTGGAACCAACACAATGGAGACGGAAAGAGA	980	
269	K W K K K K R P R N S Y K C G T N T M E R E E	291	
981	GTGAACAGACCAAGAAAAGAGAAAAATCCATATACCTGAAAGATCTGATGAAGCCCAGCGTGTAAAAA	1050	
292	S E Q T K K R E K I H I P E R S D E A Q R V F X	315	
1051	AAGTCGAAGACATCTTCATGCGACAAAAGTGATACATGTTTTAATTAAAGAGTAAAGCCCAAAAAAA	1120	
316	S S K T S S C D K S D T C F *	329	

094-25546-102299

FIGURE 8 B

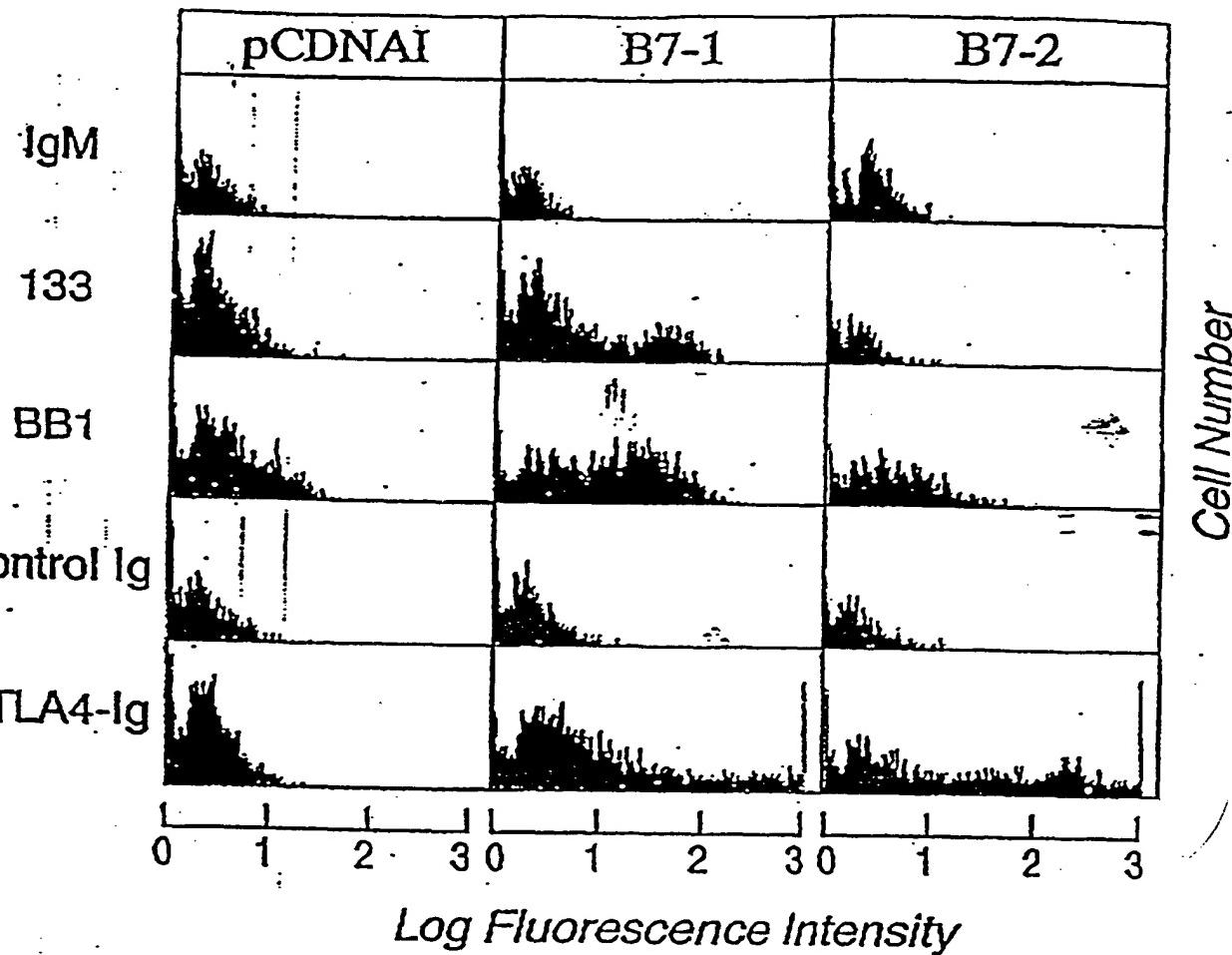
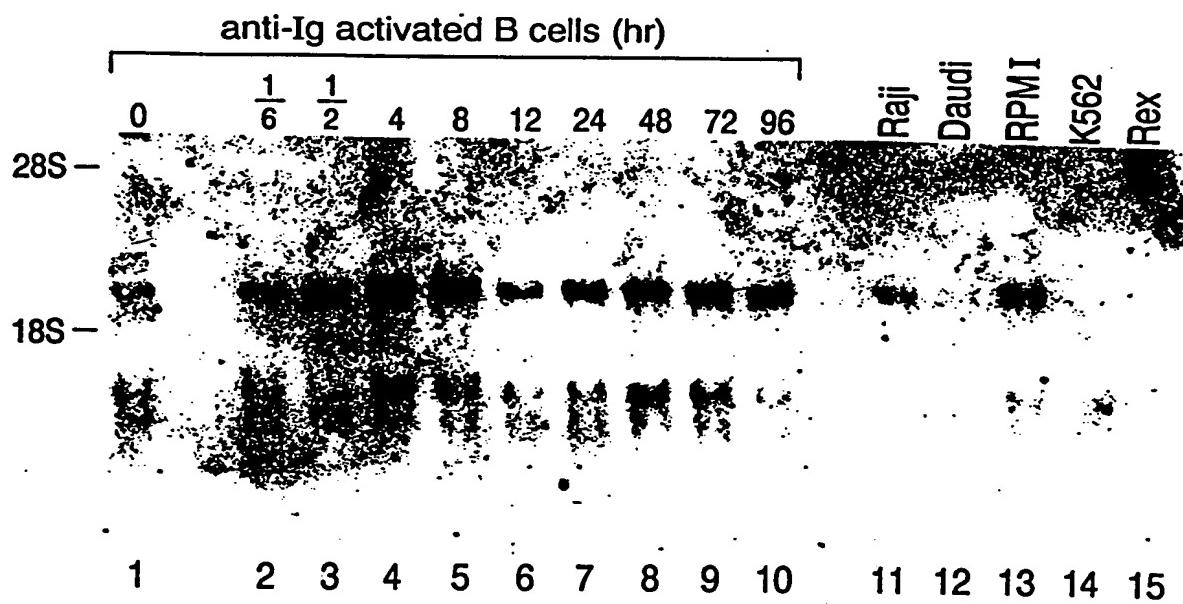
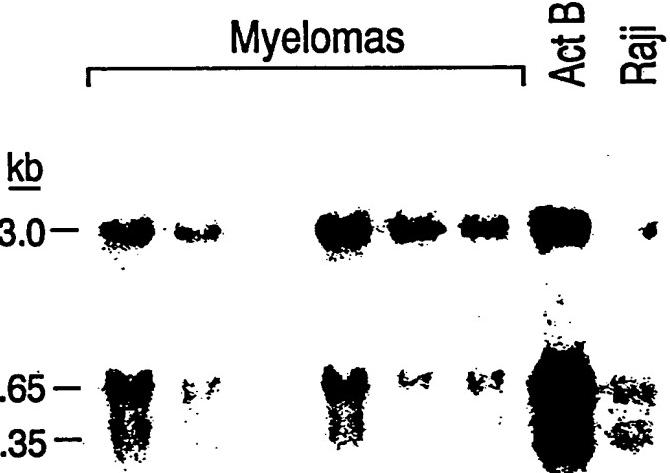


FIGURE 9



panel a

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

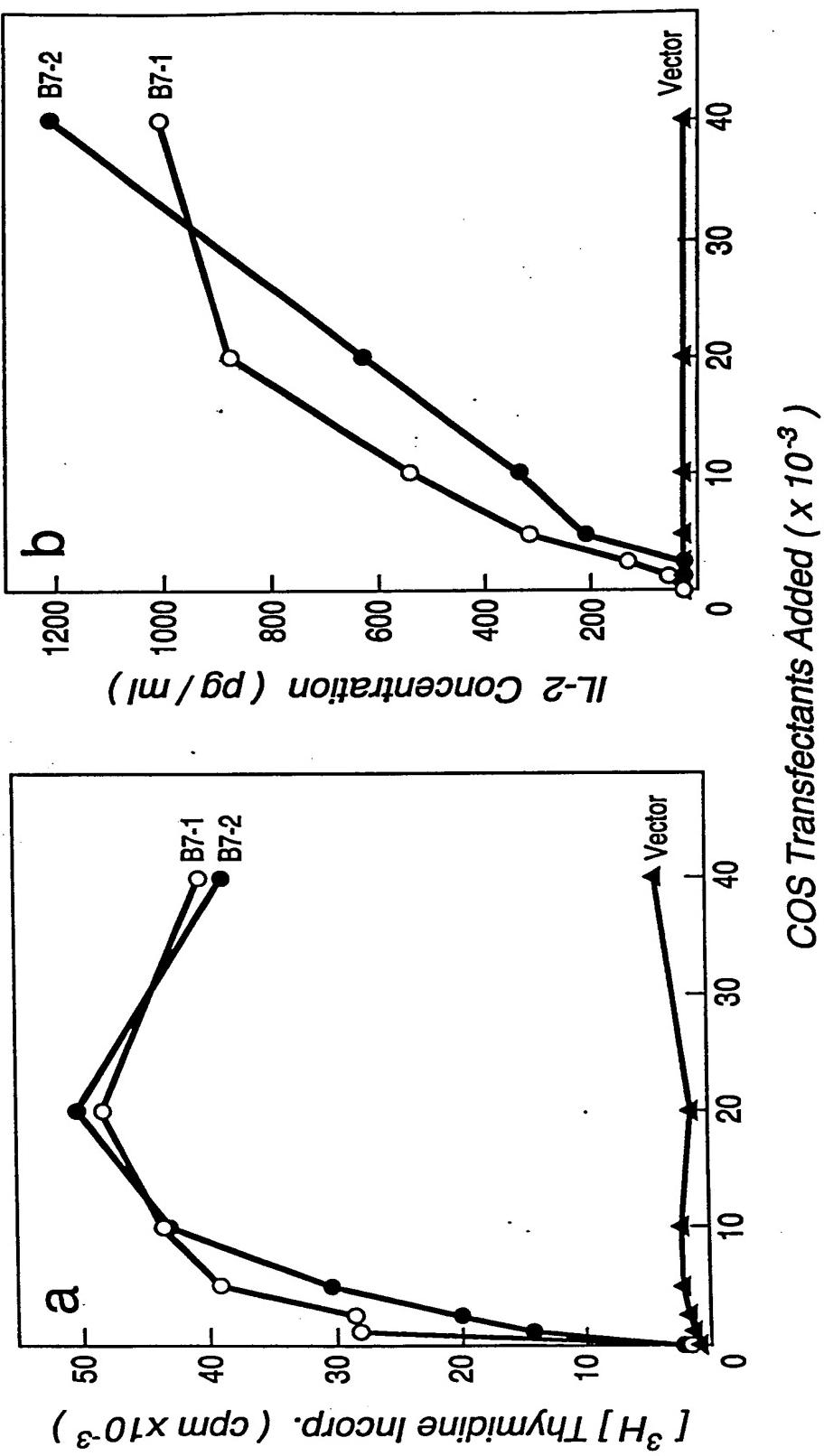


panel b

1 2 3 4 5 6 7 8

FIGURE 10

FIGURE 11



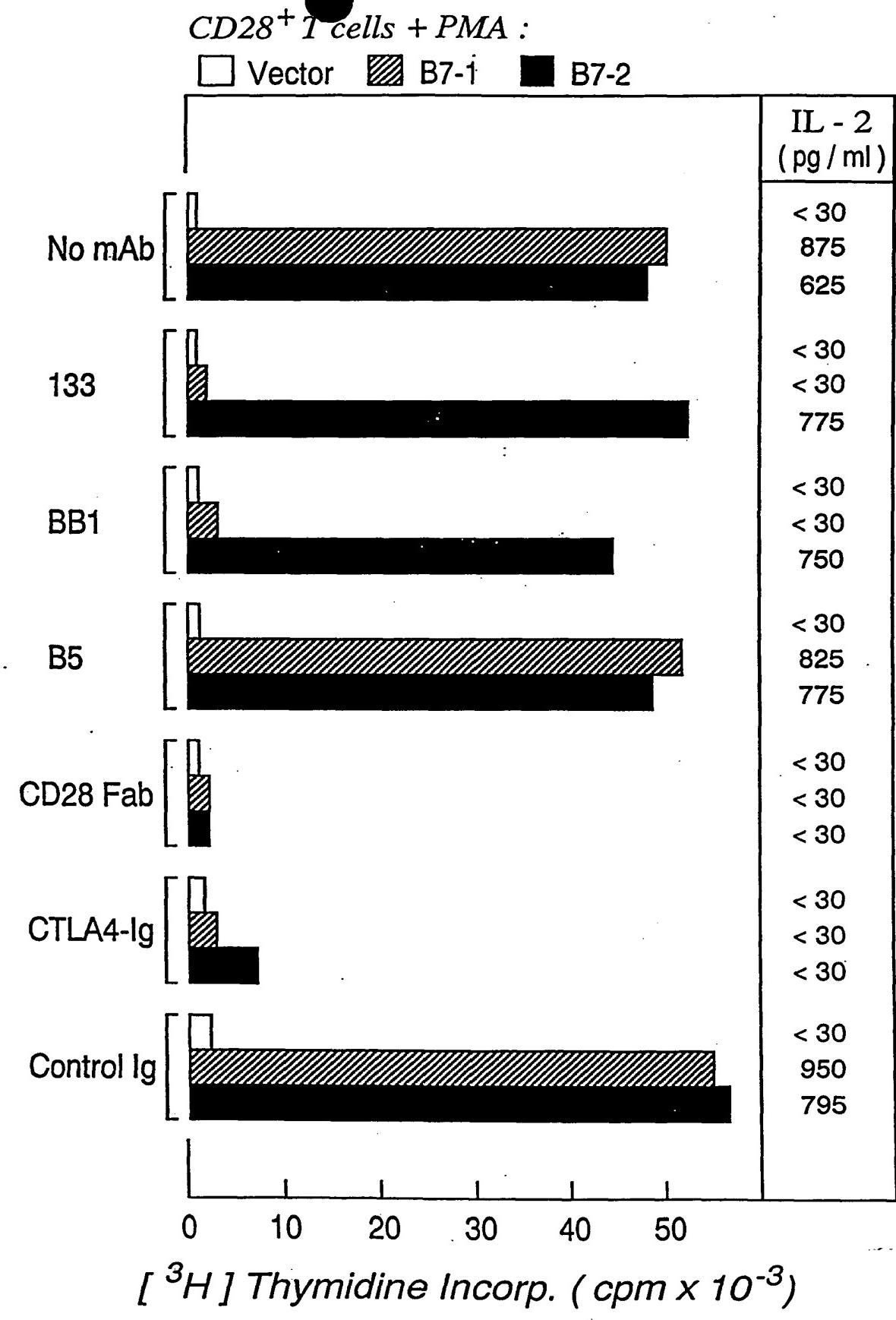


FIGURE 12

hB7-1	1	M..GHTRRQGTSPSKCPYLNFFQLLV.LAGLSHFCSGV.IHVTKEVKEVA	46
hB7-2	1	M.....DPOCTMGLSN.....ILFVMAFLLSGA...APLKIQAYFNETA	36
mB7	1	MACNCQLMQDTPLLKFPCPRLILLFVLLIRLSQVSSDVDEQLSKSVKDKV	50
.			
hB7-1	47	TLSCGHNVSVEE.LAQTRIYWQKEKKMVLT.MMSGDMNI...WPEYKNRT	91
hB7-2	37	DLPQCQFANSQNQSLSELVVFWQDQENLVNEVYLGKEKFDSVHSKYMGR	86
mB7	51	LLPCRY.NSPHEDESEDRIYWQKHDKVVLS.VIAGKLKV...WPEYKNRT	95
.			
hB7-1	92	IFDITNNLSIVIALRPSDEGYECVVLKYEKDAFKREHLAEVTLSVKAD	141
hB7-2	87	SFD.SDSWTLLRLHNLQIKDKGLYQCIIIHHKKPTGMIRIHQMNSELSVLAN	135
mB7	96	LYDNTT.YSLIILGLVLSDRGTYSCVVQKKERGTYEVKHLALVKLSIKAD	144
.			
hB7-1	142	FPTPSISDFEIPTSNI.RRIICSTSGGFPEPH....LSWLENCEELNAIN	186
hB7-2	136	FSQPEIVPISNITENVYINLTCSIIHGYPEPKKMSVLLRTKNSTIEYDGI	185
mB7	145	FSTPNITESGNPSADT.KRITCFASGGFPKPR....FSWLENGRELPGIN	189
.			
hB7-1	187	TTVSQDPETELYAVSSKLDNF...MTTNHSFMCLIKYGHLRVNQTFNWNT	233
hB7-2	186	MQKSQDNVTELYDVSISLSVSFPDVTSNMTIFCILETDKTRLLSSPFSIE	235
mB7	190	TTISQDPESELYTISSQLDFN...TTRNHTIKCLIKYGDAHVSEDFTWEK	236
.			
hB7-1	234	TKQEHF.PDNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRNERLRR	282
hB7-2	236	.LEDPPPPPDIWPWITAVLP....TVIICVMVFCLILWKWKKKRPRNSY	280
mB7	237	PPEDPPDSKNTLVLFGAGFGAVITVVVIVVIICKFCCKHRSCFRRNEA.SR	285
.			
hB7-1	283	ESVRPV*	288
hB7-2	281	KCG...TNTMERESEEQTKKREKIHIPERSDEAQRFVKSSKTSSCDKSDT	327
mB7	286	ETNNNSLTFGPEEALAEQTVFL*	306
.			
hB7-2	328	CG*	329

FIGURE 13

CCCACGGTCCGGGAGCAAGCAGACCGTAAGAGTGGCTCCTGTAGGCAGCACGGACTTG
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 GGGTGCAGGCCCTCGTCGCTCGCATTCTCACCGAGGACATCGTCGTGCCCTGAAC

AACAAACCAGACTCCTGTAGACGTGTTCCAGAACCTACGGAAGCACCACGATGGACCCC
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 TTGTTGGTCTGAGGACATCTGACAAGGTCTTGAATGCCTCGTGGGTGCTACCTGGGT

M D P R -

GATGCACCATGGGCTTGGCAATCCTTATCTTGTGACAGTCTGCTGATCTCAGATGCTG
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 CTACGTGGTACCGAACCGTTAGGAATAGAAACACTGTCAGAACGACTAGAGTCTACGAC

C T M G L A I L I F V T V L L I S D A V -

TTTCCGTGGAGACGCAAGCTTATTCATGGACTGCATATCTGCCGTGCCATTACAA
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 AAAGGCACCTCTCGCTCGAATAAAAGTACCCGTACGTATAGACGGCACGGTAAATGTT

S V E T Q A Y F N G T A Y L P C P F T K -

AGGCTCAAAACATAAGCCTGAGTGAGCTGGTAGTATTTGGCAGGACCAGCAAAAGTTGG
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 TCCGAGTTTGTATTGGACTCACTCGACCATCATAAAACCGTCTGGTCGTTCAACC

A Q N I S L S E L V V F W Q D Q Q K L V -

TTCTGTACGAGCACTATGGGCACAGAGAAACTTGATAGTGTGAATGCCAAGTACCTGG
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 AAGACATGCTCGTGTATAACCCGTCTCTTGAACATCACACTTACGGTTATGGACC

L Y E H Y L G T E K L D S V N A K Y L G -

GCCGCACGAGCTTGACAGGAACAACGGACTCTACGACTTCACAATGTCAGATCAAGG
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 CGGCGTGTGAAACTGTCTTGTGACCTGAGATGCTGAAGTGTACAGTCTAGTTCC

R T S F D R N N W T L R L H N V Q I K D -

ACATGGGCTCGTATGATTGTTTATACAAAAAAAGCCACCCACAGGATCAATTATCCTCC
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 TGTACCCGAGCATAACTAACAAATATGTTTTCGGTGGGTGCTAGTTAATAGGAGG

M G S Y D C F I Q K K P P T G S I I L Q -

AACAGACATTAACAGAACTGTCAGTGATGCCAACCTCAGTGAACCTGAAATAAAACTGG
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 TTGTCTGTAATTGCTTGACAGTCACTAGCGGTTGAAGTCACTGGACTTTATTTGACC

Q T L T E L S V I A N F S E P E I K L A -

CTCAGAATGTAACAGGAATTCTGGCATAAATTGACCTGCACGTCTAACAGTCACC
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 GAGTCTTACATTGCTCTTAAGACCGTATTAAACTGGACGTGCAGATTGTTCCAGTGG

Q N V T G N S G I N L T C T S K Q G H P -

FIGURE 14 A

CGAAACCTAAGAAGATGTATTTCTGATAACTAATTCAACTAATGAGTATGGTGATAACA
 601 -----+-----+-----+-----+-----+-----+-----+ 660
 GCTTTGGATTCTCTACATAAAAGACTATTGATTAAGTTGATTACTCATACCACTATTGT

 K P K K M Y F L I T N S T N E Y G D N M -

 TGCAGATATCACAAAGATAATGTCACAGAACTGTTCACTATCTCCAAACAGCCTCTCTCTT
 661 -----+-----+-----+-----+-----+-----+-----+ 720
 ACGTCTATAGTGTCTATTACAGTGTCTGACAAGTCATAGAGGTTGTCGGAGAGAGAAA

 Q I S Q D N V T E L F S I S N S L S L S -

 CATTCCCGATGGTGTGGCATATGACCCTGTGTCTGGAAACGGAGTCATGA
 721 -----+-----+-----+-----+-----+-----+-----+ 780
 GTAAGGGCCTACCACACACCGTATACTGGCAACACACACAAGACCTTGCCCTCAGTTACT

 F P D G V W H M T V V C V L E T E S M K -

 AGATTTCCCTCAAACCTCTCAATTCACTCAAGAGTTCCATCTCCTCAAACGTATTGGA
 781 -----+-----+-----+-----+-----+-----+-----+ 840
 TCTAAAGGAGGTTGGAGAGTTAAAGTGAGTTCTCAAAGGTAGAGGAGTTGCATAACCT

 I S S K P L N F T Q E F P S P Q T Y W K -

 AGGAGATTACAGCTTCAGTTACTGTGGCCCTCCTCTGTGATGCTGCTCATATTGTAT
 841 -----+-----+-----+-----+-----+-----+-----+ 900
 TCCTCTAATGTCGAAGTCATGACACACGGGAGGAGGAACACTACGACGAGTAGTAAACATA

 E I T A S V T V A L L L V M L L I I V C -

 GTCACAAGAACCGAATCAGCCTAGCAGGCCAGCAACACAGCCTCTAAAGTTAGAGCGGG
 901 -----+-----+-----+-----+-----+-----+-----+ 960
 CAGTGTCTCGGCTTAGTCGGATCGTCCGGTCTGTGTCGGAGATTCAATCTCGCCC

 H K K P N Q P S R P S N T A S K L E R D -

 ATAGTAACGCTGACAGAGAGACTATCAACCTGAAGGAACCTGAACCCAAATTGCTTCAG
 961 -----+-----+-----+-----+-----+-----+-----+ 1020
 TATCATTGCGACTGTCTCTGATAGTTGGACTTCCTGAACTTGGGTTAACGAAGTC

 S N A D R E T I N L K E L E P Q I A S A -

 CAAAACCAAATGCAGAGTGAAGGCAGTGAGAGCCTGAGGAAAGAGTTAAAAATTGCTTTG
 1021 -----+-----+-----+-----+-----+-----+-----+ 1080
 GTTTTGGTTTACGTCTCACTCCGTCACTCTCGGACTCCTTCTCAATTAAACGAAAC

 K P N A E *

 CCTGAAATAAGAAGTGCAGAGTTCTCAGAATTCAAAATGTTCTCAGCTGATTGAAATT
 1081 -----+-----+-----+-----+-----+-----+-----+ 1140
 GGACTTTATTCTCACGTCTCAAAGAGTCTTAAGTTTACAAGAGTCGACTAACCTAA

 CTACAGTTGAATAATTAAAGAAC
 1141 -----+-----+-----+-----+-----+-----+-----+ 1163
 GATGTCAACTTATTAATTCTTG

FIGURE 14 B

B.CTLA4 Competition on hB7.2
Competitors: hB7.1,hB7.2,hB7.2V,hB7.2C

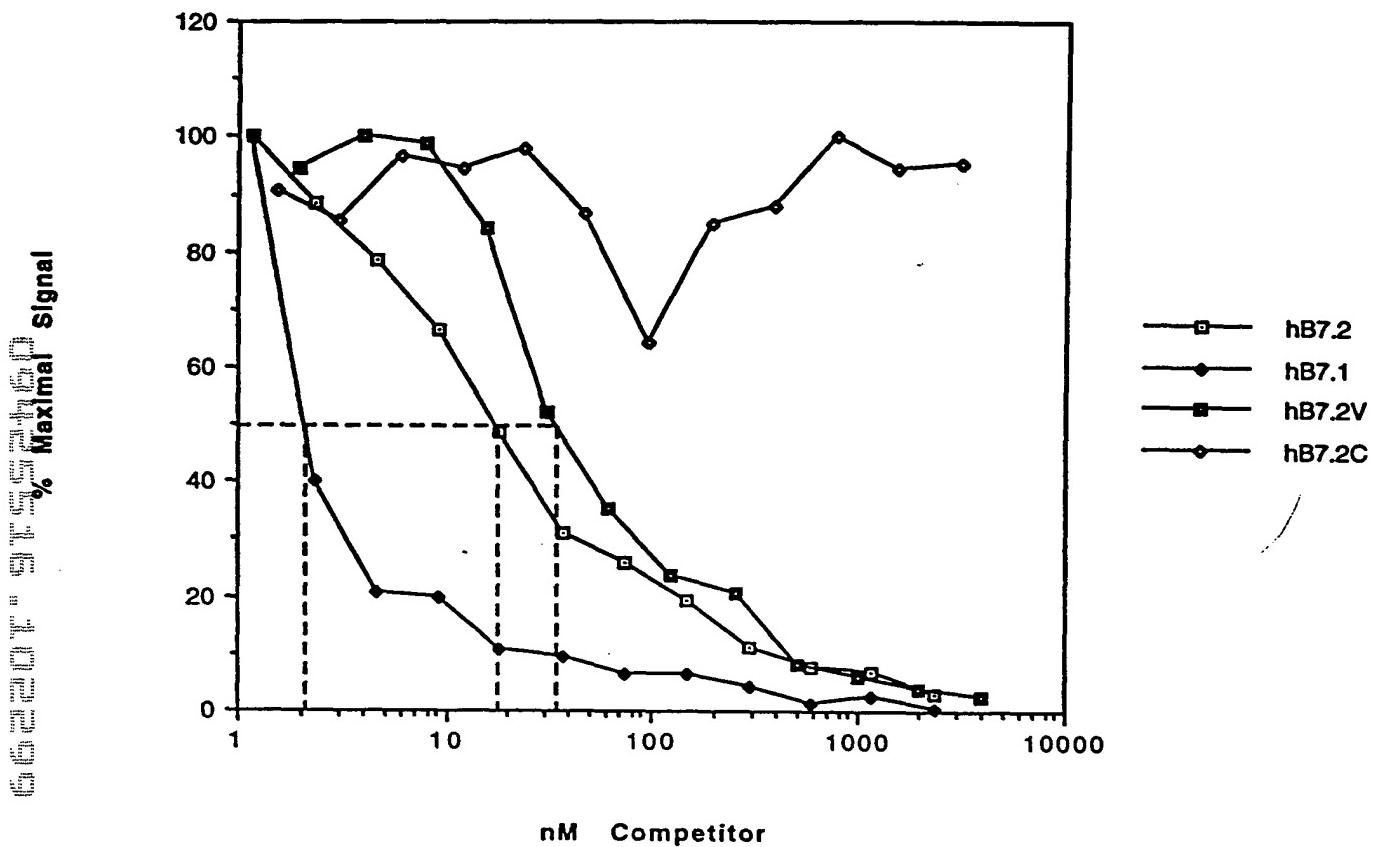


FIG. 15

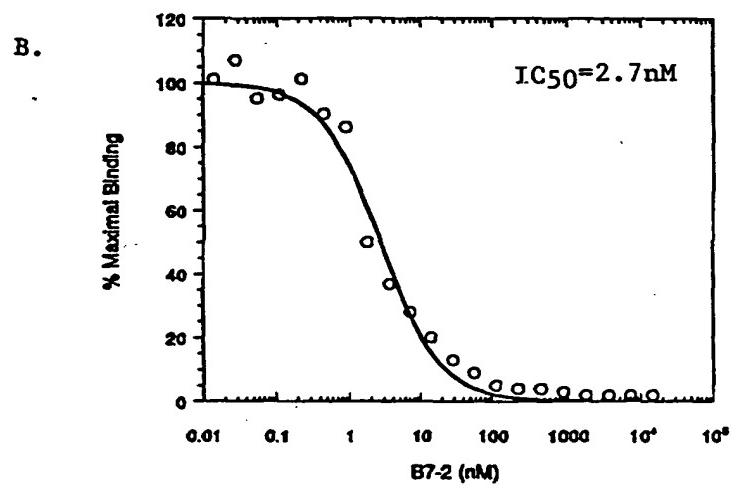
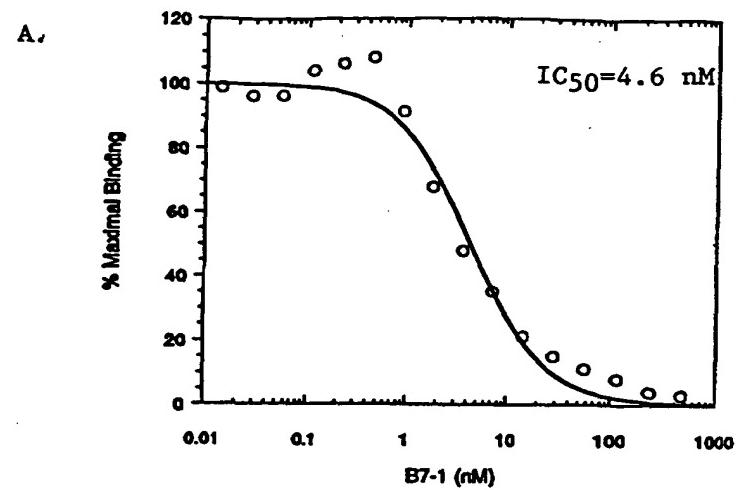
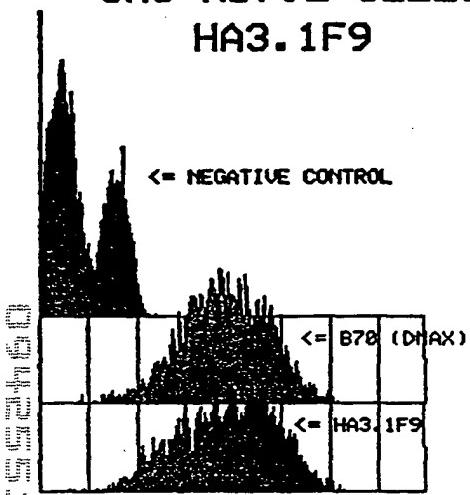


FIG. 16

#11:/23/HAHF003\FL1-H\FL1-Height

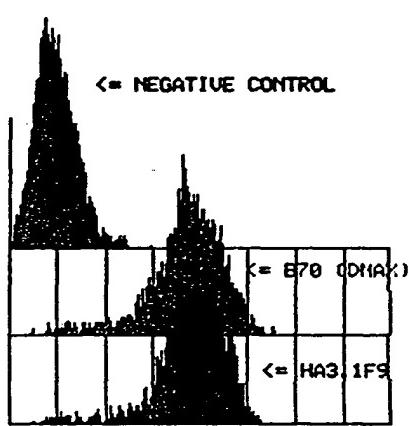
**CHO-HB7.2 CELLS
HA3.1F9**



#11:/23/HAHF020\FL1-H\FL1-Height

**3T3-HB7.2 CELLS
HA3.1F9**

B.



#11:/23/HAHF037\FL1-H\FL1-Height

**3T3-NEO CELLS
HA3.1F9**

C.

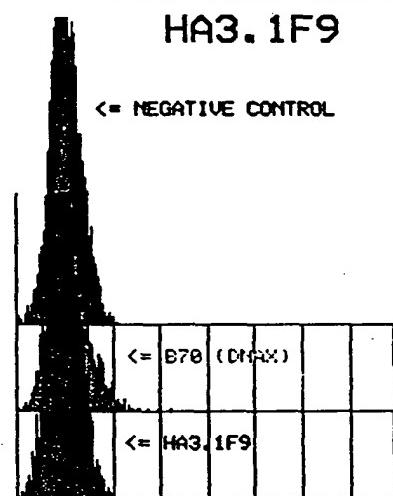
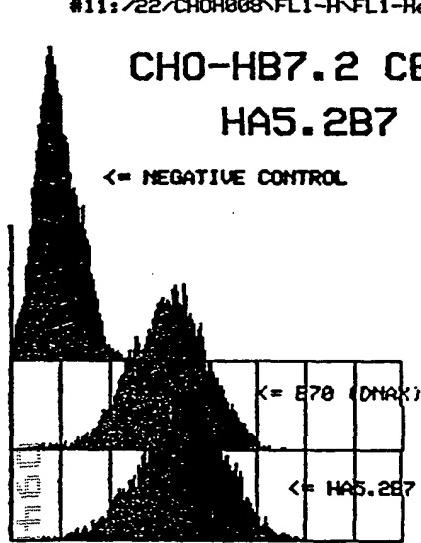


FIG. 17

#11:/22/CHOH008\FL1-H\FL1-Height

**CHO-HB7.2 CELLS
HA5.2B7**

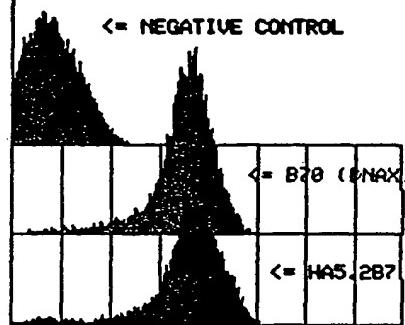
<= NEGATIVE CONTROL



#11:/22/3T3H008\FL1-H\FL1-Height

**3T3-HB7.2 CELLS
HA5.2B7**

<= NEGATIVE CONTROL



#11:/22/3T3008\FL1-H\FL1-Height

**3T3-NEO CELLS
HA5.2B7**

<= NEGATIVE CONTROL

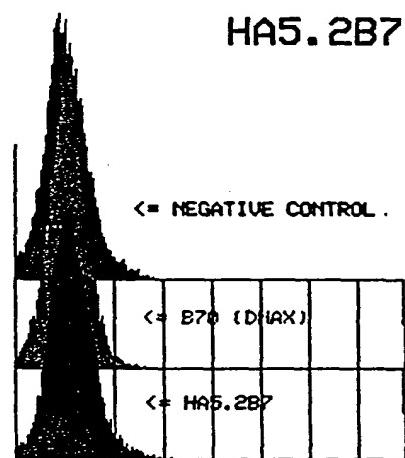
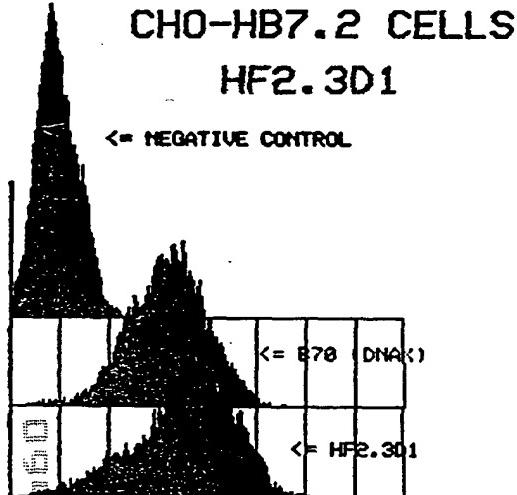
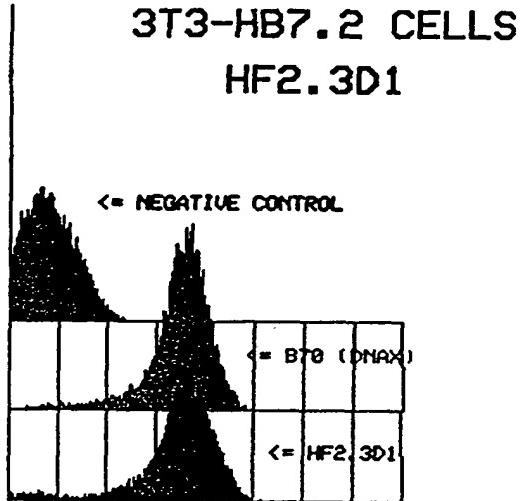


FIG. 18

#11:/22/CHOH003\FL1-H\FL1-Height



#11:/22/3T3H003\FL1-H\FL1-Height



#11:/22/3T3H003\FL1-H\FL1-Height

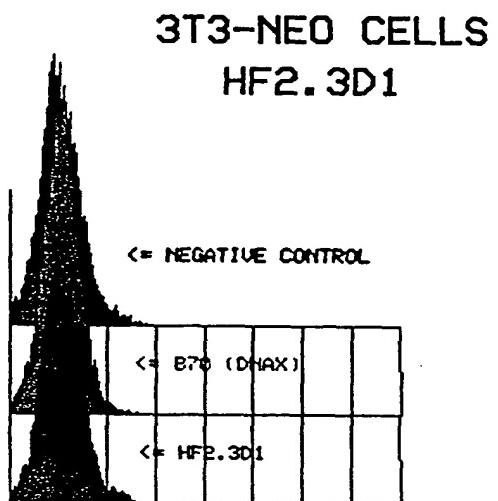


FIG. 19

Binding of Modified Forms of B7 Family Members to CTLA4

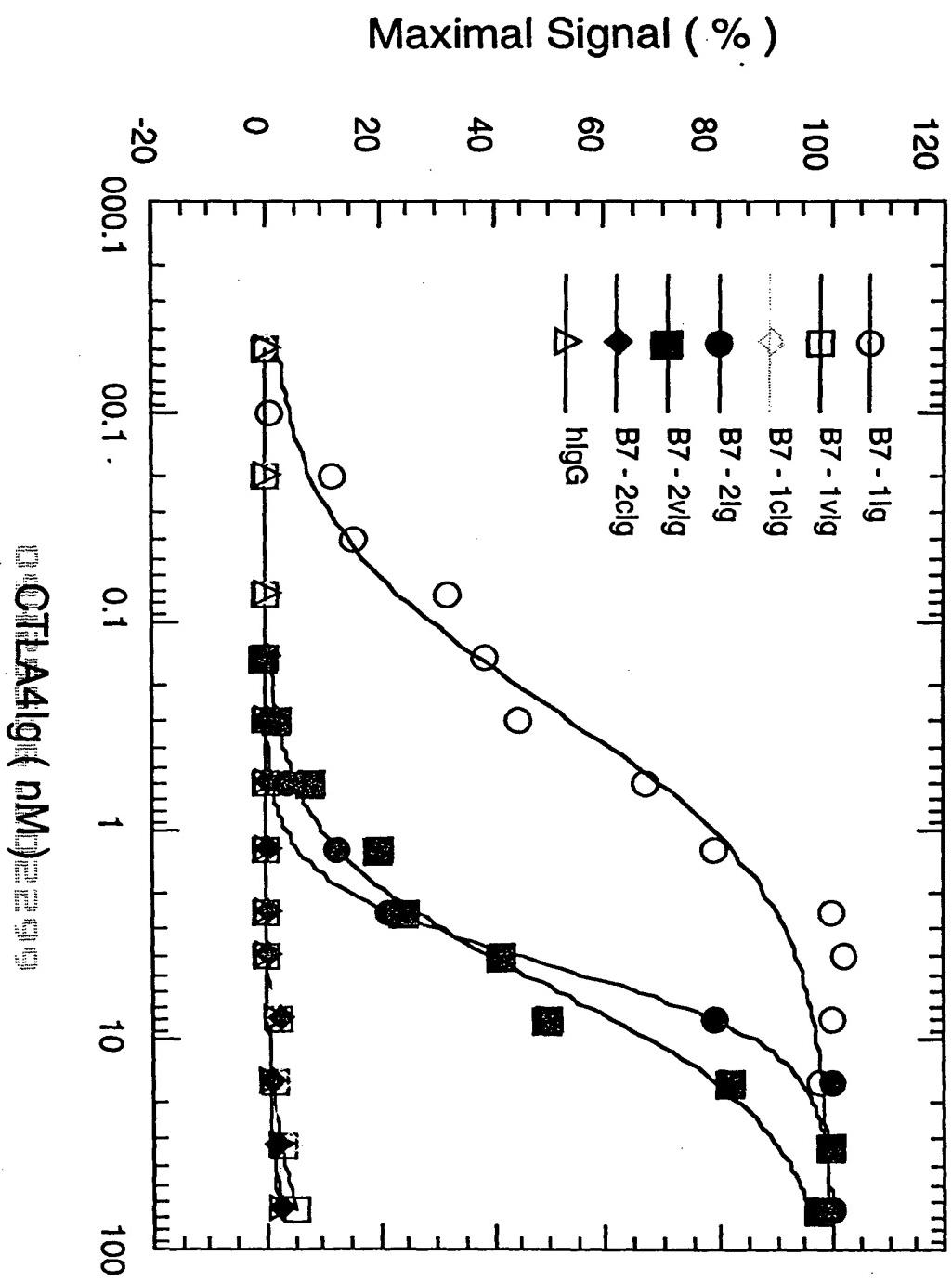


FIGURE 20

SELECTED PREFERENCES: Arithmetic/Lin ar

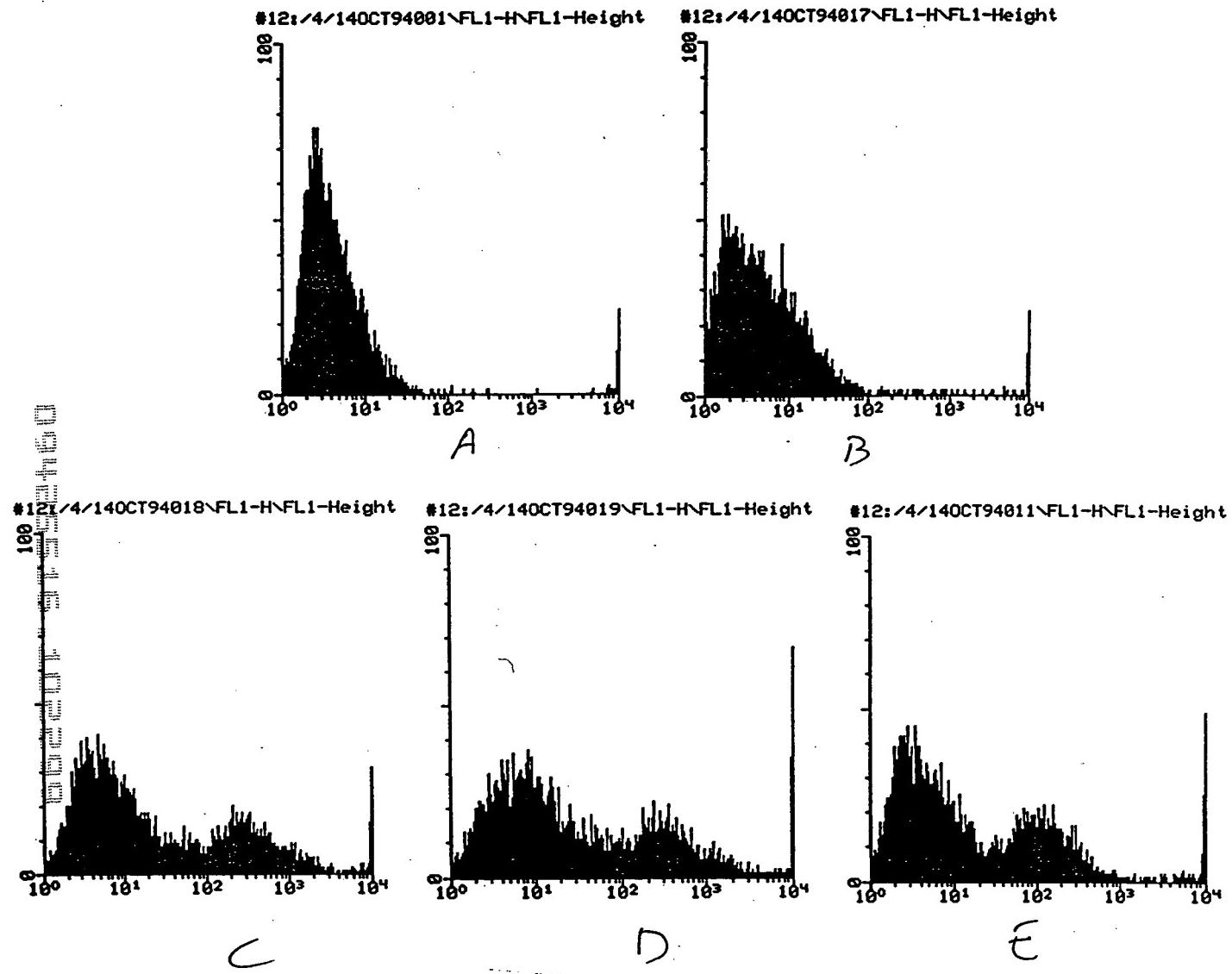


FIGURE 21

FACS Analysis of CD28 + CHO Cells Using B7 Family Members

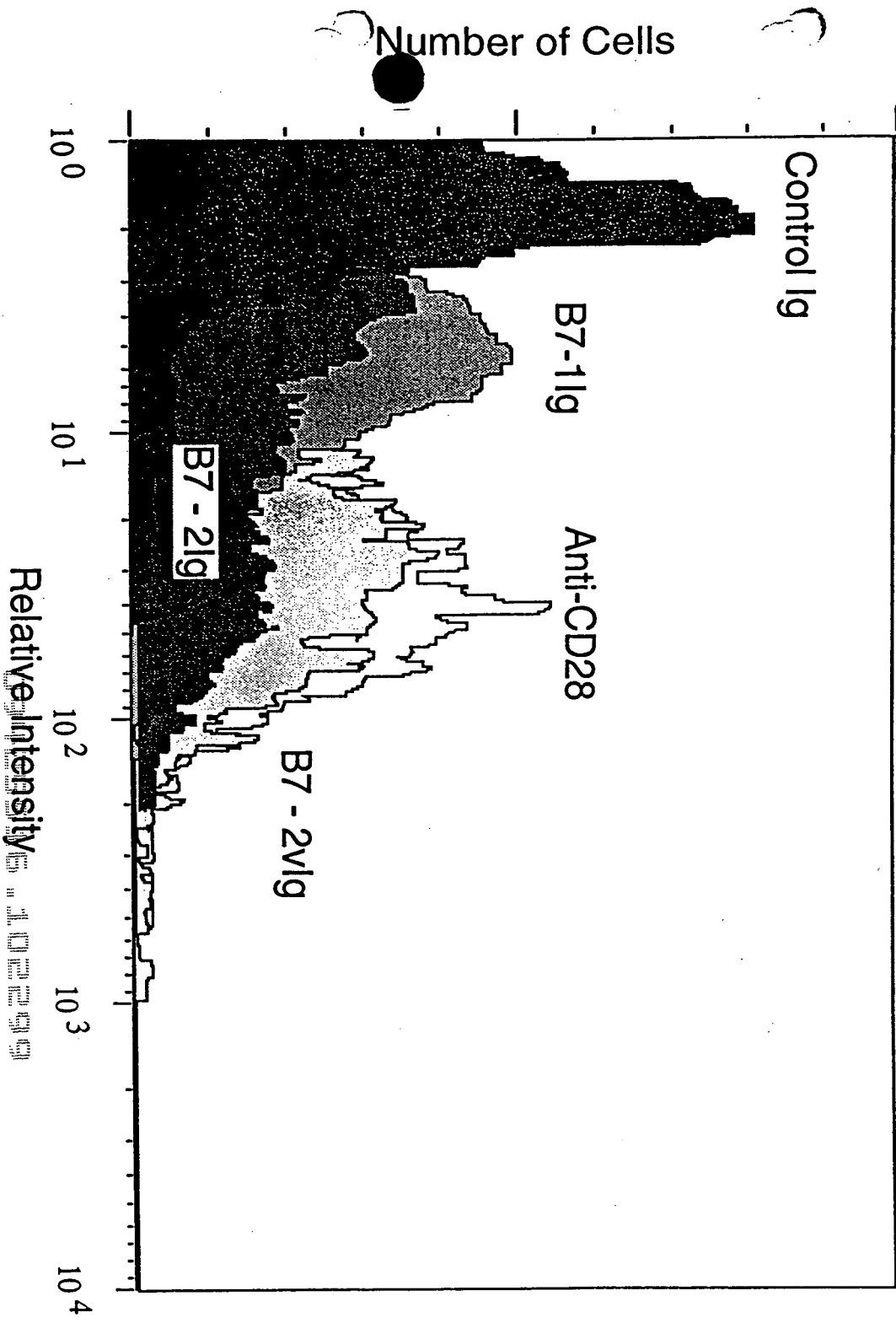


FIGURE 22

The Variable Domain of B7-2 Can Provide a Costimulatory Signal for CD28 + T Cells

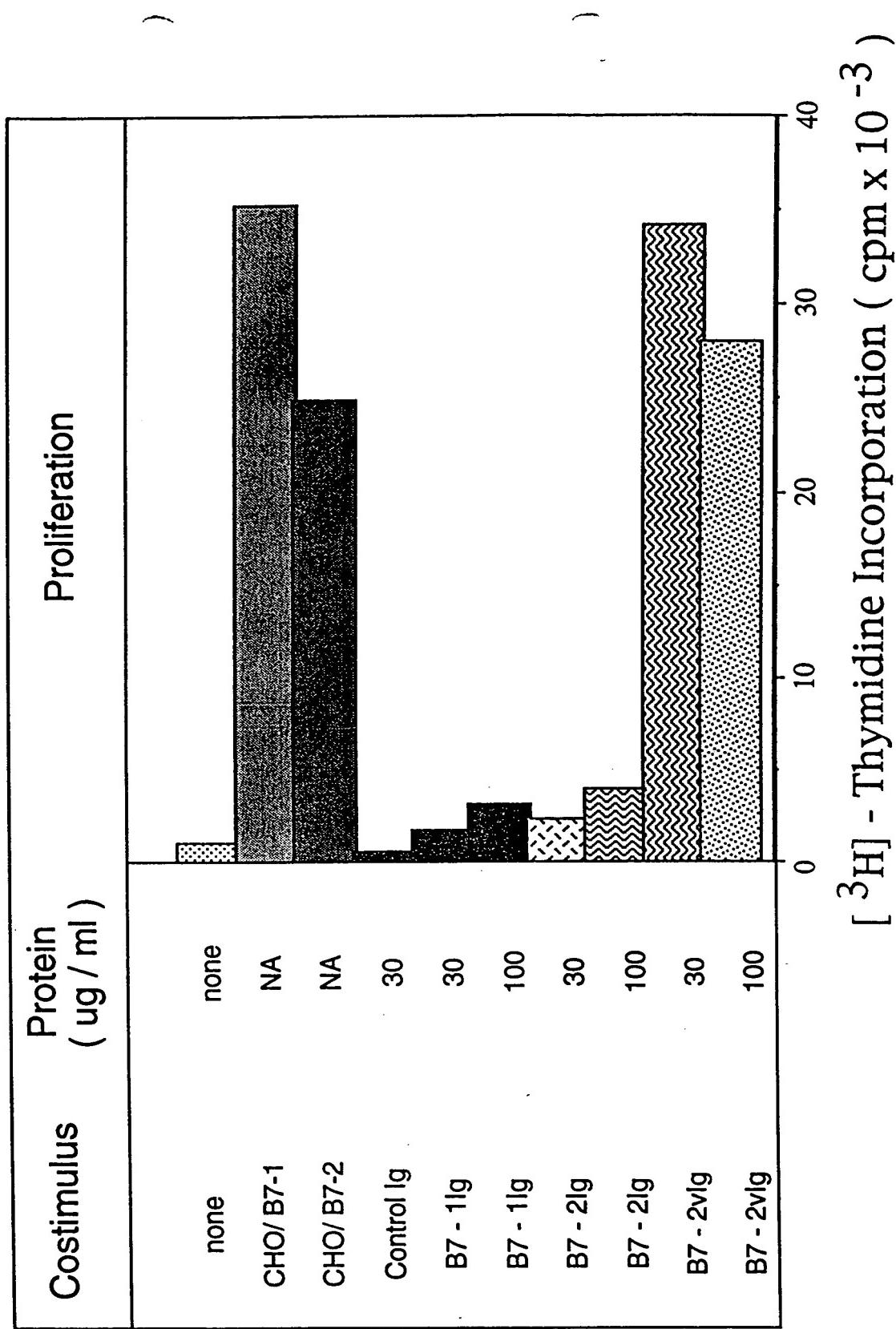


FIGURE 23

Proliferation of CD28⁺ T Cells to Costimulation by Soluble Proteins Prepared from B7 Family Members

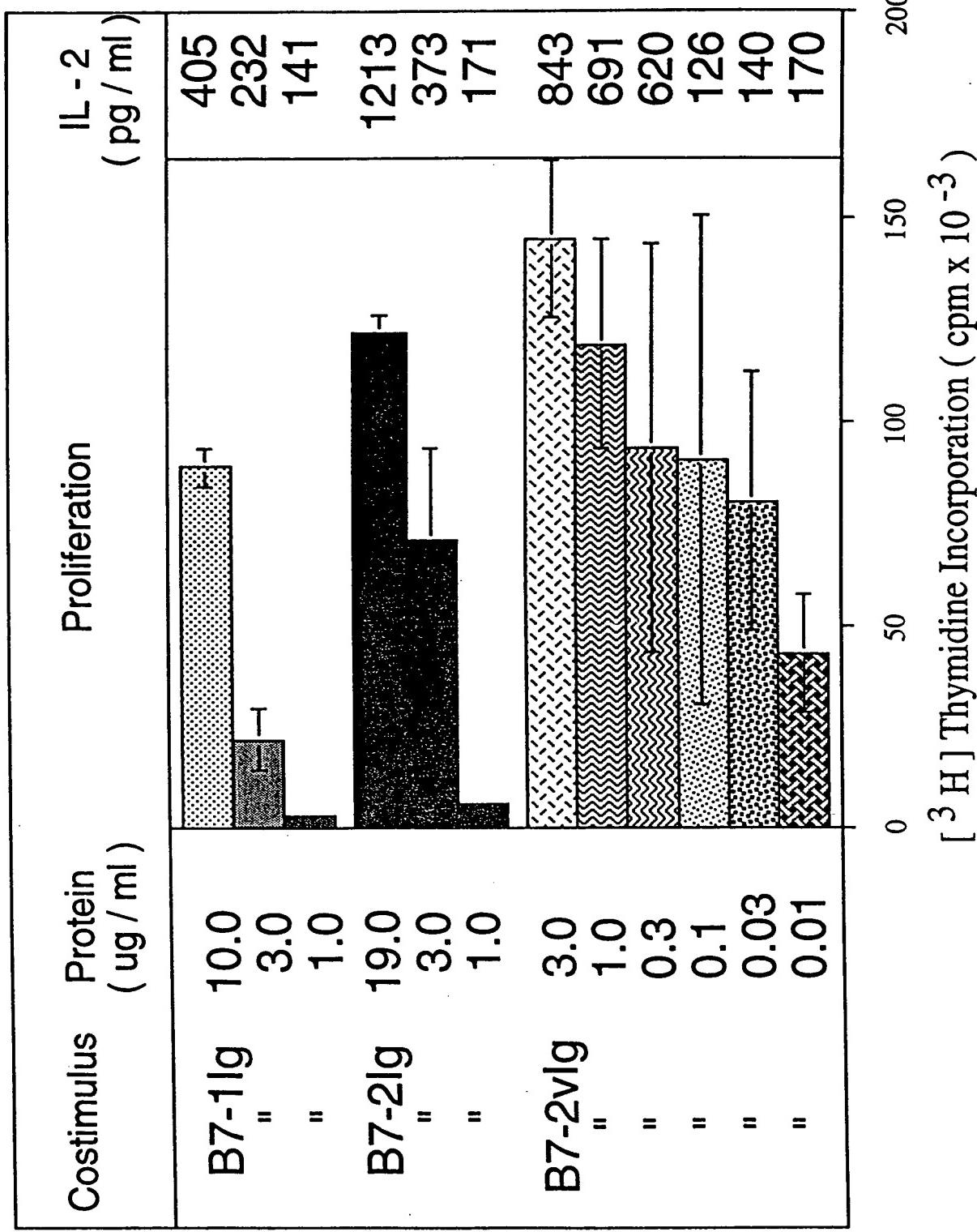


FIGURE 24

Costimulation by B7-2vlg Induces Increased IL-2 Secretion

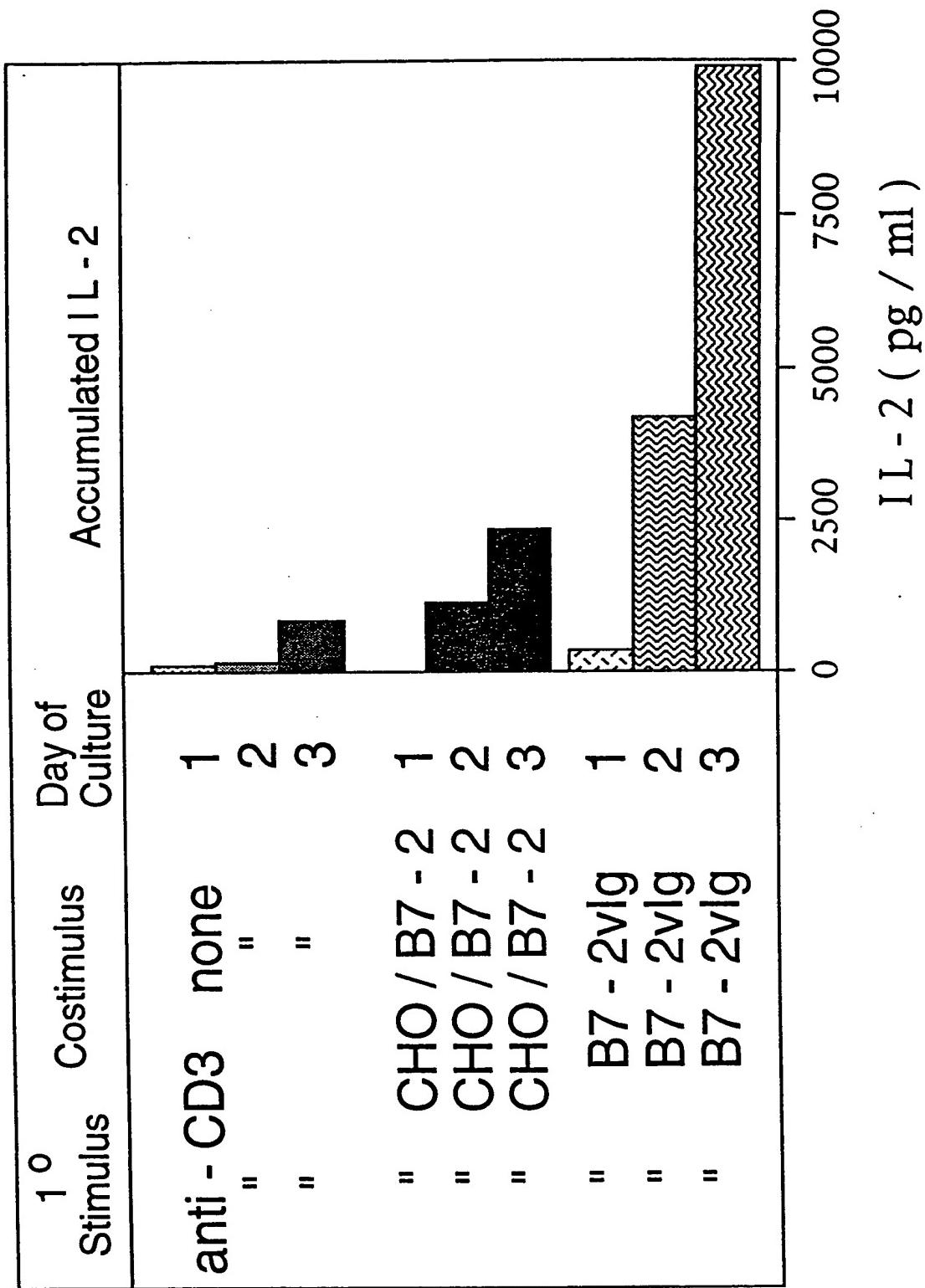


FIGURE 25

Costimulation of T Cells by Soluble B7 Family Members Induces IL-2 Secretion

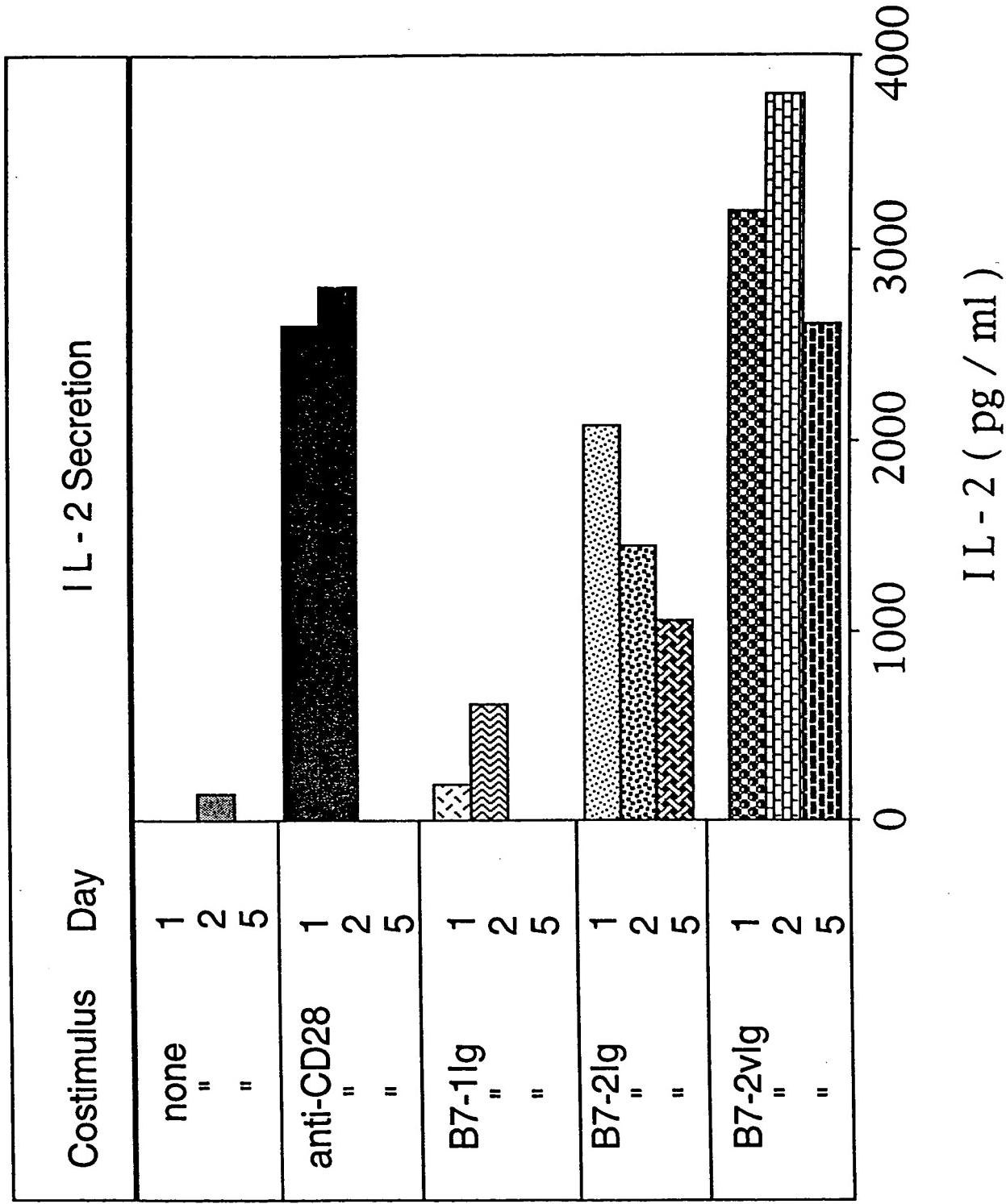


FIGURE 26

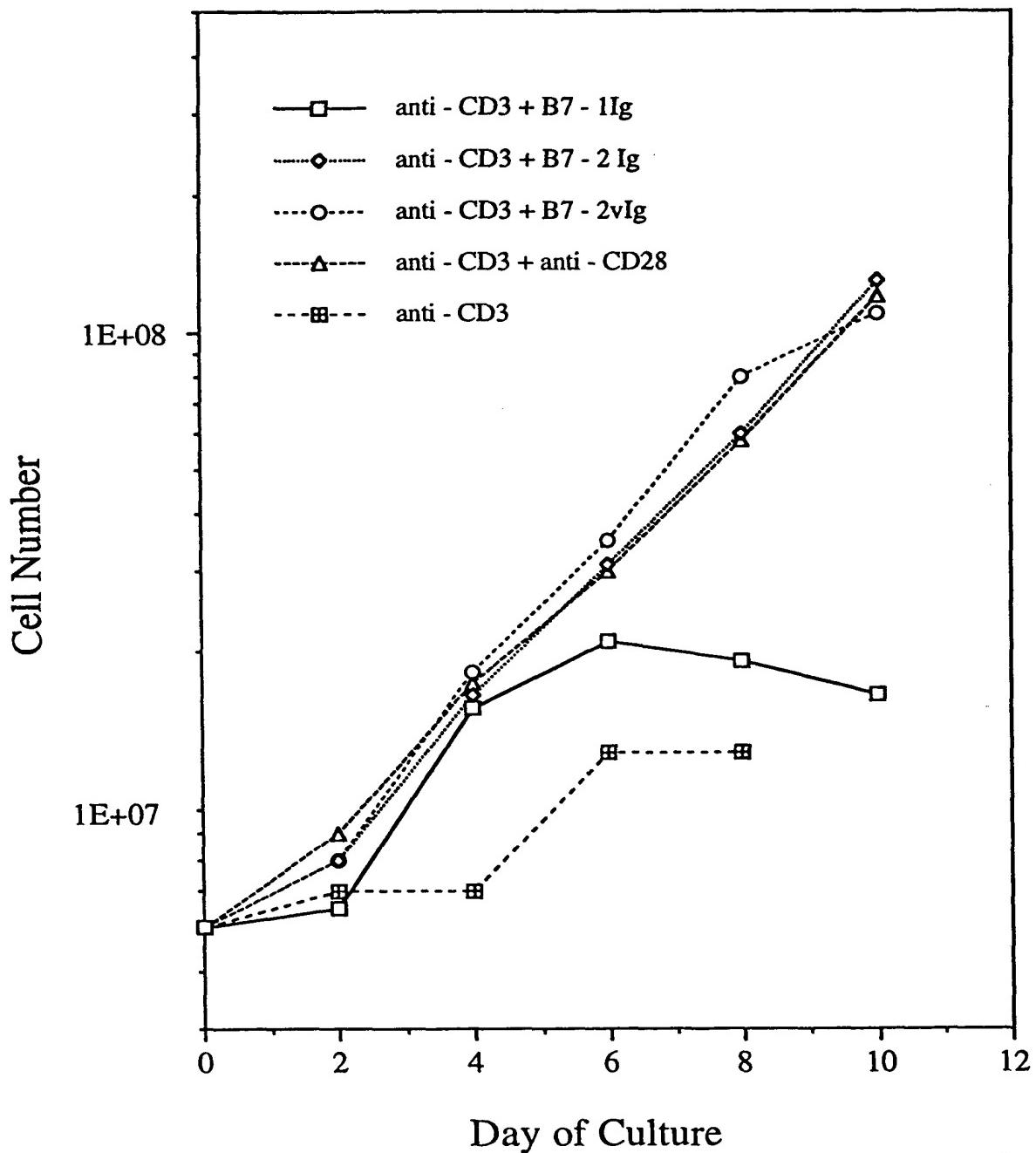


FIGURE 27